In the Claims

Please amend the claims as follows. Deleted text is indicated in ~~strikeout~~, and newly added text is indicated in underline and **bold** typeface.

1. (Canceled)

2. (Previously Amended) The method according to claim 37, wherein the primer is a fragment of deoxyribonucleic or ribonucleic acid, an oligodeoxyribonucleotide, an oligoribonucleotide, or a copolymer of deoxyribonucleic acid and ribonucleic acid.

E1

3. (Previously Amended) The method according to claim 37, wherein the nucleic acid of interest is deoxyribonucleic acid, a ribonucleic acid, or a copolymer of deoxyribonucleic acid and ribonucleic acid.

4. (Previously Amended) The method according to claim, 37, wherein the target nucleotide is defined as any known base, which include wild-type or a known mutant base so long as the base is known and it is desired to know its variant.

5. (Previously Amended) The method according to claim 37, wherein the terminator nucleotide is a dideoxyribonucleotide or an analogue thereof and the non-terminator nucleotide is a deoxyribonucleotide or a ribonucleotide or an analogue thereof.

6. (Previously Amended) The method according to claim 37, wherein the terminator nucleotide is unlabeled.

7. (Previously Amended) The method according to claim 37, wherein the terminator nucleotide is labeled with a detectable marker that is different form the marker on the non-terminators.

8. (Previously Amended) The method according to claim 37, wherein in step (d), the duplex from step (c) is contacted with non-terminator nucleotides, wherein each non-terminators is labeled with the same or different detectable marker.

9. (Previously Amended) The method according to claim 37, wherein said detectable marker comprises an enzyme, radioactive isotope, a fluorescent molecule, or a protein ligand.

E1 cont.

10. (Canceled)

11. (Previously Amended) The method according to claim 37, wherein said enzyme is template-dependent.

12. (Original) The method of claim 11, wherein the template-dependent enzyme is DNA polymerase.

13. (Original) The method according to claim 12, wherein the DNA of polymerase is *E. coli* DNA polymerase I or the "Klenow fragment" thereof, T4 DNA polymerase, T7 DNA polymerase, or *T. aquaticus* DNA polymerase.

14. (Original) The method according to claim 11, wherein said enzyme is RNA polymerase or reverse transcriptase.

15. (Previously amended) The method according to claim 37, wherein the primer comprises on or more moieties that permit affinity separation of the primer from the unincorporated reagent and/or the nucleic acid of interest.

16. (Previously amended) The method according to claim 37, wherein the primer comprises one or more moieties that links the primer to a solid surface.

17. (Original) The method according to claim 15, wherein the moieties comprises biotin or digitonin.

18. (Original) The method according to claim 16, wherein the moieties comprises biotin or digitonin.

19. (Original) The method according to claim 15, wherein the moieties comprises a DNA or RNA sequence that permits affinity separation of the primer from the unincorporated reagent and/or the nucleic acid of interest via base pairing to a complementary sequence present in a nucleic acid attached to a solid support.

20. (Original) The method according to claim 16, wherein the moieties comprises a DNA or RNA sequence that permits affinity separation of the primer from the unincorporated reagent and/or the nucleic acid of interest via base pairing to a complementary sequence present in a nucleic acid attached to a solid support.

21. (Original) The method according to claim 15, wherein the moieties comprises a DNA or RNA sequence that allows the primer to link to a solid support via base pairing to a complementary sequence present in solid surface.

22. (Original) The method according to claim 16, wherein the moieties comprises a DNA or RNA sequence that allows the primer to link to a solid support via base pairing to a complementary sequence present in solid surface.

23. (Previously amended) The method according to claim 37, wherein the nucleic acid of interest has been synthesized enzymatically *in vivo, in vitro,* or synthesized non-enzymatically.

24. (Previously amended) The method according to claim 37, wherein the nucleic acid of interest is synthesized by polymerase chain reaction.

E1 cont.

25. (Previously Amended) The method according to claim 37, wherein the nucleic acid of interest comprises non-natural nucleotide analogs.

26. (Original) The method according to claim 25, wherein the non-natural nucleotide analogs comprise deoxyinosine or 7-dezaz-2'-deoxyguanosine.

27. (Previously amended) The method according to claim 37, wherein the sample comprises genomic DNA from an organism, RNA transcript thereof, or cDNA prepared from RNA transcripts thereof.

28. (Previously Amended) The method according to claim 37, wherein the sample comprises extragenomic DNA from an organism, RNA transcripts thereof, or cDNA prepared from RNA transcripts thereof.

29. (Previously Amended) The method according to claim 27, wherein the organism is a plant, microorganism, bacteria, or virus.

30. (Previously Amended) The method according to claim 28, wherein the organism is a plant, microorganism, bacteria, or virus.

31. (Original) The method according to claim 27, wherein the organism is a vertebrate or invertebrate.

32. (Original) The method according to claim 28, wherein the organism is a vertebrate or invertebrate.

33. (Original) The method according to claim 27, wherein the organism is a mammal.

34. (Original) The method according to claim 28, wherein the organism is a mammal.

E1
CONT.

35. (Original) The method according to claim 27, wherein the organism is a human being.

36. (Original) The method according to claim 27, wherein the organism is a human being.

37. (Currently amended) A method for detecting or quantifying **the presence of** a target nucleic acid in a sample by detecting a signal from a plurality of labeled nucleotides incorporated into a primer **extension product** comprising:

(a) selecting a nucleic acid having a target nucleotide base at a predetermined position in a template of a nucleic acid of interest, **wherein the target nucleotide base is a mutant nucleotide base or a known wild-type nucleotide base**;

(b) preparing an unlabeled primer complementary to a sequence immediately upstream of the target nucleotide base;

(c) treating a sample containing the nucleic acid of interest, if the nucleic acid is double-stranded, so as to obtain unpaired nucleotide bases spanning the ~~specific~~ **predetermined** position, or directly employing step (d) if the nucleic acid of interest is single-stranded;

(d) annealing the primer from (b) with the ~~target~~ nucleic acid **of interest** from (c) ~~under high stringency conditions~~ to obtain a primer-nucleic acid duplex, wherein the target nucleotide base in the nucleic acid of interest is the first unpaired base immediately downstream of the 3' end of the primer;

E1
OOL

(e) mixing the primer-nucleic acid duplex from (d) with a primer extension reaction reagent comprising: (i) three types of non-terminator nucleotides that are not complementarily matched to the **known wild-type** target nucleotide, wherein at least one type of the non-terminator nucleotide is labeled with a detectable marker; and optionally (ii) one type of terminator nucleotide that is complementarily matched to the **known wild-type** target nucleotide, wherein the terminator nucleotide is not labeled;

(f) ~~performing~~ **extending** the primer extension reaction by enzymatic or chemical means **to form a labeled primer extension product comprising a plurality of labeled non-terminator nucleotides, wherein a labeled primer extension product does not form when the target nucleotide base is wild-type** ~~, wherein the incorporation of said non-terminator nucleotide and optionally, the terminator nucleotide, to the primer depends upon the identity of the unpaired nucleotide base in the nucleic acid template, and wherein when the target nucleotide is changed to any other type of nucleotide, a plurality of non-terminator nucleotides~~

~~labeled with said detectable marker are sequence dependently incorporated into the primer extension~~; and

(g) determining the presence of the ~~other type of~~ **mutant target** nucleotide at the predetermined position in the nucleic acid of interest by detecting the presence of ~~detectable signal of non-terminator nucleotides extended from~~ the **labeled** primer **extension product, wherein detecting the labeled primer extension product is not based on size**~~, without employing gel electrophoresis size separation method~~.

38. (Canceled)

E!
COU+.

39. (New) A method for detecting the presence of a nucleic acid, comprising:

providing a nucleic acid having a known wild-type target nucleotide base or a mutant target nucleotide base at a predetermined position;

annealing a primer to the nucleic acid immediately 3' of the predetermined position;

extending the primer in one extension reaction to form a labeled primer extension product using a reaction mixture comprising non-terminator nucleotides, wherein at least one non-terminator nucleotide is complementarily matched to the mutant target nucleotide base and at least one non-terminator nucleotide is labeled with a detectable marker; and wherein a labeled primer extension product does not form when the target nucleotide base is wild-type; and

detecting the presence of the labeled primer extension product; and

correlating the presence of the labeled primer extension product with the presence of a mutant target nucleotide base in the nucleic acid.

40. (New) A method for detecting the presence of a mutant nucleotide in a nucleic acid, comprising:

providing a nucleic acid having a known wild-type target nucleotide base or a mutant target nucleotide base at a predetermined position;

annealing a primer to the nucleic acid immediately 3' of the predetermined position;

extending the primer to form a labeled primer extension product using a reaction mixture comprising non-terminator nucleotides, wherein the non-terminator nucleotides are not complementarily matched to the known wild-type target nucleotide base and at least one non-terminator nucleotide is labeled with a detectable marker; and wherein a labeled primer extension product does not form when the target nucleotide base is wild-type; and

detecting the presence of the labeled primer extension product, wherein the detection of the labeled primer extension product is not based on the size of the labeled extension product, and wherein detecting a labeled primer extension product indicates the presence of a mutant nucleotide in the nucleic acid.

41. (New) A method for detecting or quantifying the presence of a target nucleic acid in a sample by detecting a signal from a plurality of labeled nucleotides incorporated into a primer extension product comprising:

(a) selecting a nucleic acid having a target nucleotide base at a predetermined position in a template of a nucleic acid of interest, wherein the target nucleotide base is a known mutant nucleotide base or a known wild-type nucleotide base;

(b) preparing an unlabeled primer complementary to a sequence immediately upstream of the target nucleotide base;

(c) treating a sample containing the nucleic acid of interest, if the nucleic acid is double-stranded, so as to obtain unpaired nucleotide bases spanning the predetermined position, or directly employing step (d) if the nucleic acid of interest is single-stranded;

(d) annealing the primer from (b) with the nucleic acid of interest from (c) to obtain a primer-nucleic acid duplex, wherein the target nucleotide base in the nucleic acid of interest is the first unpaired base immediately downstream of the 3' end of the primer;

(e) mixing the primer-nucleic acid duplex from (d) with a primer extension reaction reagent comprising: (i) at least one types of non-terminator nucleotides that are not complementarily matched to the known mutant target nucleotide base, wherein at least one type of the non-terminator nucleotide is labeled with a detectable marker; and optionally (ii) one type of terminator nucleotide that is complementarily matched to the known mutant target nucleotide base, wherein the terminator nucleotide is not labeled;

(f) extending the primer extension reaction by enzymatic or chemical means to form a labeled primer extension product comprising a plurality of labeled non-terminator nucleotides, wherein a labeled primer extension product does not form when the target nucleotide base is mutant; and

(g) determining the presence of the wild-type target nucleotide at the predetermined position in the nucleic acid of interest by detecting the presence of the labeled nucleotide in primer extension product, wherein detecting the labeled nucleotide primer extension product is not based on size.